

SEQUENCE LISTING

<110> GOODNOW, Jr., Robert Alan
MARK, David Fu-Chi
MARTIN, Mitchell Lee
ROSINSKI, James Andrew

<120> Sequence #115 as a target for identifying weight modulating compounds

<130> 21366

<140>
<141>

<150> US 60/436,375
<151> 2002-12-23

<160> 6

<170> PatentIn version 3.2

<210> 1
<211> 1011
<212> DNA
<213> Mus musculus

<220>
<221> GPCR #115
<222> (1)..(1011)
<223> CHR7-36867

<400> 1
atgaactcgt gggacgcggg cctggcgggg ctactggtgg gcacgatggg cgtctcgtcg 60
ctgtccaacg cgctggtgct gctctgcctg ctgcacagcg cggacatccg ccgccaggcg 120
ccggcgctct tcacctgaa cctcacgtgc gggaacctgc tgtgcaccgt ggtcaacatg 180
ccgctcacgc tggccggcgt cgtggcgcag cggcagccgg cgggcgaccg cctgtgccgc 240
ctggctgcct tcctcgacac ctctctggct gccaaactcca tgctcagcat ggccgcgctc 300
agcatcgacc gctgggtggc cgtggtcttc ccgctgagct accggggcaa gatgcgcctc 360
cgcgacgcgg cgctcatggt ggcttacacg tggctgcacg cgctcacctt ccagccgcgc 420
gcgctcgccc tgtctgggt cggcttccac cagctgtacg cctcgtgcac gctgtgcagc 480
cggcggccag acgagcgcct gcgcttcgcc gtcttcactg gcgccttcca cgctctcagc 540

```

ttcctgctct ccttcgtcgt gctctgctgc acgtacctca aggtgctcaa ggtggccgc 600
ttccattgca agcgcatcga cgtgatcacc atgcagacgc tgggtgctgct ggtggacctg 660
caccccagtg tgcgggaacg ctgtctggag gacgagaagc ggagggcgaca gcgagccacc 720
aagaagatca gcaccttcac agggaccttc cttgtgtgct tcgcgcccta tgtgatcacc 780
aggctagtgg agctcttctc cacgggtgcc atcggtccc actgggggggt gctgtccaag 840
tgcttggcgt acagcaaggc cgcacccgac ccttttgtgt actccttact gcgacaccag 900
taccgcaaaa gctgcaagga gattctgaac aggtcctctgc acagacgctc catccactcc 960
tctggcctca caggcgactc tcacagccag aacattctgc cgggtgtctga g 1011

```

```

<210> 2
<211> 337
<212> PRT
<213> Mus musculus

```

```

<220>
<221> GPCR #115
<222> (1)..(337)

```

```

<400> 2

```

```

Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Met
1          5          10          15

```

```

Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His
          20          25          30

```

```

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
          35          40          45

```

```

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
          50          55          60

```

```

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
65          70          75          80

```

```

Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
          85          90          95

```

Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu
100 105 110

Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala
115 120 125

Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu
130 135 140

Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser
145 150 155 160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe
165 170 175

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr
180 185 190

Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val
195 200 205

Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Leu His Pro Ser Val
210 215 220

Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr
225 230 235 240

Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro
245 250 255

Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly
260 265 270

Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala
275 280 285

Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser
290 295 300

Cys Lys Glu Ile Leu Asn Arg Leu Leu His Arg Arg Ser Ile His Ser
 305 310 315 320

Ser Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser
 325 330 335

Glu

<210> 3
 <211> 1172
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> GPCR #115
 <222> (1)..(1172)
 <223> Q9QXI3

<400> 3
 ctgaacgcca tcagcgggcg cgcacccatga actcgtggga cgcggggcctg gcgggggctgc 60
 tgggtgggcac aatcggcgtg tcgctgctgt ccaacgggct ggtgctgctc tgccctcctgc 120
 acagcgtgta catccgccgc caggcgccgg cgcctttcac tctcaacctc acgtgtggca 180
 acctgctgtg taccgtggtc aacatgccac taacactggc cggcgtcgtg gcacaacggc 240
 agccggccgg ggaccgcctg tgcgcctgg ccgccttctt cgacaccttt ctggccgcca 300
 actccatgct cagtatggcc gcgctcagca tcgaccgtg ggtggctgtg gtcttccgc 360
 tgagctaccg tgccaagatg cgcctccgag atgcgcctt catggtggcc tacacgtggc 420
 tgcacgcgt cactttcccg gccaccgcgc tcgccctgtc ctggctcggc ttccaccagc 480
 tgtatgcctc gtgcacgctg tgcagccggc ggcccgacga gcgcctgcgc tttgctgtct 540
 tcaccagcgc cttccatgag cttagcttcc tgctctcctt catcgtgctc tgcttcacgt 600
 acctcaaggt gctcaaggtg gcccgtttcc actgcaagcg catcgacgtg atcaccatgc 660
 agacgctcgt gctgttagtg gacatccatc ccagtgtgag ggaacgatgt ctggagggaac 720
 agaagcggag gcggcagcgt gccaccaaga agatcagcac cttcataggg accttccctcg 780

tgtgctttgc accctatgtg attaccaggc tgggtggaact cttctccaca gcacccattg 840
 actcacactg ggggtgtgctg tccaagtgtt tggcctacag caaggctgct tctgaccct 900
 tcgtgtactc cttgctgcga caccagtacc gcaggagctg caaggagctt ctgaacagga 960
 tcttcaacag acgctccatt cactctgtgg gcctcacagg tgactctcac agccagaaca 1020
 ttctgccagt gtcggaatga aggacagctc tctgtttggg gagttcagaa tgaggtggcc 1080
 agagcagagg gaggtggtct gggactcctg ggtggacagg aactgccacc attgtctggc 1140
 gattgacatg atgctgatgt ctgaacaaga tc 1172

<210> 4
 <211> 337
 <212> PRT
 <213> Rattus norvegicus

<220>
 <221> GPCR #115
 <222> (1)..(337)

<400> 4

Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Ile
 1 5 10 15

Gly Val Ser Leu Leu Ser Asn Gly Leu Val Leu Leu Cys Leu Leu His
 20 25 30

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
 35 40 45

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
 50 55 60

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
 65 70 75 80

Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
 85 90 95

Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu

100	105	110
Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Phe Met Val Ala		
115	120	125
Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu		
130	135	140
Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser		
145	150	155
Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe		
165	170	175
His Ala Leu Ser Phe Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr		
180	185	190
Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val		
195	200	205
Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Ile His Pro Ser Val		
210	215	220
Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr		
225	230	235
Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro		
245	250	255
Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Asp		
260	265	270
Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala		
275	280	285
Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser		
290	295	300
Cys Lys Glu Leu Leu Asn Arg Ile Phe Asn Arg Arg Ser Ile His Ser		

taccgcaaaa gctgcaagga gattctgaac aggctcctgc acagacgctc catccactcc 960

tctggcctca caggcgactc tcacagccag aacattctgc cgggtgtctga gtga 1014

<210> 6
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> GPCR #115
<222> (1)..(337)

<400> 6

Met Asn Ser Trp Asp Ala Gly Leu Ala Gly Leu Leu Val Gly Thr Met
1 5 10 15

Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His
20 25 30

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
35 40 45

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
50 55 60

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
65 70 75 80

Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
85 90 95

Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu
100 105 110

Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala
115 120 125

Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu
130 135 140

Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser
 145 150 155 160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe
 165 170 175

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr
 180 185 190

Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val
 195 200 205

Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Leu His Pro Ser Val
 210 215 220

Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr
 225 230 235 240

Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro
 245 250 255

Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly
 260 265 270

Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala
 275 280 285

Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser
 290 295 300

Cys Lys Glu Ile Leu Asn Arg Leu Leu His Arg Arg Ser Ile His Ser
 305 310 315 320

Ser Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser
 325 330 335

Glu